

What is claimed is:

1. A method for identifying a compound that modulates gene expression, which comprises:

- (a) contacting a chromatin assembled DNA containing a gene of interest with
 - (1) a SWI/SNF chromatin remodeling complex containing BRG-1 ATPase, or a portion of the remodeling complex,
 - (2) a transcription factor containing a tryptophan cluster or a leucine zipper, or a fragment of the transcription factor, and
 - (3) a test compound; and
 - (b) determining whether there is an increase or decrease in chromatin remodeling of the DNA containing the gene of interest in the presence and absence of the test compound, whereby a test compound that increases or decreases chromatin remodeling relative to the chromatin remodeling in the absence of the test compound is identified as a compound that modulates gene expression, or
- determining whether there is an increase or decrease in transcription of the gene of interest in the presence and absence of the test compound, whereby a test compound that increases or decreases transcription relative to the transcription in the absence of the test compound is identified as a compound that modulates gene expression.

2. The method of claim 1, wherein the increase or decrease in chromatin remodeling is determined by analyzing one or more DNaseI hypersensitive sites in the DNA containing the gene of interest.

3. The method of claim 1, wherein the transcription factor contains a leucine zipper, or a fragment thereof.

4. The method of claim 3, wherein the transcription factor is c-fos, c-jun, or C/EBP α , or a fragment thereof.

5. The method of claim 3, wherein the transcription factor is phosphorylated CREB, or a fragment thereof.
6. The method of claim 1, wherein the gene of interest is a cAMP-responsive gene.
7. The method of claim 1, wherein the transcription factor contains a tryptophan cluster, or a fragment thereof.
8. The method of claim 7, wherein the transcription factor is IRF-1, or a fragment thereof.
9. A method for identifying a compound that modulates gene expression, which comprises:
 - (a) contacting a chromatin assembled DNA containing a gene of interest with
 - (1) a SWI/SNF chromatin remodeling complex containing BRG-1 ATPase, or a portion of the remodeling complex,
 - (2) a transcription factor fragment consisting of a C4 motif or C2H2 motif from a zinc finger domain, and
 - (3) a test compound; and
 - (b) determining whether there is an increase or decrease in chromatin remodeling of the DNA containing the gene of interest in the presence and absence of the test compound, whereby a test compound that increases or decreases chromatin remodeling relative to the chromatin remodeling in the absence of the test compound is identified as a compound that modulates gene expression, or
determining whether there is an increase or decrease in transcription of the gene of interest in the presence and absence of the test compound, whereby a test compound that increases or decreases transcription relative to the transcription in the absence of the test compound is identified as a compound that modulates gene expression.

10. The method of claim 9, wherein the increase or decrease in chromatin remodeling is determined by analyzing one or more DNaseI hypersensitive sites in the DNA containing the gene of interest.

11. A method for identifying a compound that modulates gene expression, which comprises:

- (a) contacting a chromatin assembled DNA containing a gene of interest with
 - (1) a SWI/SNF chromatin remodeling complex containing BRM ATPase, or a portion of the remodeling complex,
 - (2) a transcription factor or fragment thereof, and
 - (3) a test compound; and
- (b) determining whether there is an increase or decrease in chromatin remodeling of the DNA containing the gene of interest in the presence and absence of the test compound, whereby a test compound that increases or decreases chromatin remodeling relative to the chromatin remodeling in the absence of the test compound is identified as a compound that modulates gene expression, or
determining whether there is an increase or decrease in transcription of the gene of interest in the presence and absence of the test compound, whereby a test compound that increases or decreases transcription relative to the transcription in the absence of the test compound is identified as a compound that modulates gene expression.

12. The method of claim 11, wherein the increase or decrease in chromatin remodeling is determined by analyzing one or more DNaseI hypersensitive sites in the DNA containing the gene of interest.

13. The method according to claim 11, wherein the transcription factor contains an ankyrin repeat.

14. The method according to claim 13, wherein the transcription factor is ICD22 or CBF-1, or a fragment thereof.

15. The method according to claim 11, wherein the gene of interest is a Notch receptor regulated gene.

16. A compound identified by the method of claim 1 that modulates gene expression.

17. A compound identified by the method of claim 9 that modulates gene expression.

18. A compound identified by the method of claim 11 that modulates gene expression.